

Docket No.: 01017/42148

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AUG 21 2006

REMARKS**I. The Rejection under 35 U.S.C. § 101 Should be Withdrawn**

The Examiner rejected claims 2-3 and 7-18 under 35 U.S.C. § 101 asserting that the claims are directed to non-statutory subject matter. Claim 2 is amended to recite "isolated nucleic acid," and claims 7-9 and 11 are amended to recite "recombinant vectors." The host cells recited in claims 13-14 comprise the recombinant vector of claims 7-9 and 11. These amendments indicate that the claimed products are touched by the hand of man and therefore are statutory subject matter. Claims 3, 9, 10, 12, 16 and 18 are cancelled without prejudice. Therefore, the rejection of claims 2, 7, 8, 11, 13, 14 and 17 under 35 U.S.C. § 101 should be withdrawn.

II. The Rejection under 35 U.S.C. § 112, First Paragraph Should be Withdrawn

The Examiner rejected claims 13-18 under 35 U.S.C. § 112, first paragraph for allegedly failing to comply with the written description requirement. In particular, the Examiner asserted that the claims encompass *in vivo* cells of any transgenic non-human multicellular organism and the specification does not provide an adequate written description of transgenic animals. The terms "host cells" and "transgenic animals" are adequately described in the specification. One of skill in the art understands that the term "host cell" refers to cells used in molecular biology techniques such as DNA cloning, to receive, maintain, and allow the reproduction of recombinant DNA vectors and expression of recombinant proteins, to name a few. The specification provides many species encompassed by the genus of "host cells" (see, e.g. pages 27-29 of the specification). In addition, the specification describes the use of non-human mammals encoding the TP2 gene. (See, e.g. page 12, lines 15-25).

The Examiner also rejected claims 13-18 under 35 U.S.C. § 112, first paragraph for allegedly not being enabled by the specification. In particular, the Examiner asserted that the specification does not enable transgenic animal cells *in vivo*. The process for preparing transgenic non-human mammals are well known in the art. Further, the specification refers to the methods described in U.S. Patent No. 5,489,743 and PCT Patent Application No. WO 94/28122. (See page 12, lines 21-25). Thus, claims 12-18 are enabled by the teachings in the specification.

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In view of the foregoing amendment and remarks, claims 13, 14, and 17 are adequately described and enabled by the specification. Therefore, the rejection under 35 U.S.C. § 112, first paragraph should be withdrawn.

III. The Rejection Under 35 U.S.C. § 112, Second paragraph Should be Withdrawn

Claims 29 and 30 were rejected under 35 U.S.C. § 112, second paragraph as allegedly being indefinite for failing to particular point out and distinctly claim the subject matter of the invention. Claims 29 and 30 are amended to recite "the amino acid position at 868 of SEQ ID NO: 20" rather than SEQ ID NO: 19. As SEQ ID NO: 19 is a polynucleotide sequence that comprises nucleotides rather than amino acids, the reference to SEQ ID NO: 19 was a typographical error. In view of the foregoing amendment, the rejection of claims 29 and 30 under 35 U.S.C. § 112, second paragraph should be withdrawn.

IV. The Rejection Under 35 U.S.C. § 102 Should be Withdrawn

Claims 1, 4, 6, 7, 12, 13, 16, 18-20 and 26-27 were rejected under 35 U.S.C. § 102(e) as allegedly being anticipated by Cech *et al*, U.S. Patent No. 6,626,836 (denoted herein as Cech '836). The Examiner stated the polynucleotide sequence of SEQ ID NO: 224 of Cech '836 is identical to nucleotides 13-3798 of SEQ ID NO: 19 of the present invention. Amended claims 1, 26 and 27 are directed to the nucleotide sequence of SEQ ID NO: 13, SEQ ID NO: 19, and nucleotide sequence encoding the amino acid sequence of SEQ ID NO: 14 or SEQ ID NO: 20. The polynucleotide sequence of SEQ ID NO: 224 in Cech '836 is not 100% identical to the claim-recited polynucleotide sequences of SEQ ID NO: 13 and SEQ ID NO: 19. (See attached alignments in Exhibit A). In addition, the amino acid sequence of SEQ ID NO: 225, which is encoded by the polynucleotide sequence of SEQ ID NO: 223 is not 100% identical to the full length amino acid sequence of SEQ ID NO: 14 or SEQ ID NO: 20. (See attached alignments in Exhibit B). Claims 4, 6, 12, 16 and 18-20 are canceled without prejudice. Therefore, the amended claims are not anticipated by the polynucleotide sequence of SEQ ID NO: 224 in Cech '836 and the rejection of claims 1, 13, 26 and 27 under 35 U.S.C. § 102(c) should be withdrawn.

The Examiner also rejected claims 28-30 under 35 U.S.C. § 102(e) as allegedly being anticipated by Cech *et al*, U.S. Patent No. 6,475,789 (denoted herein as Cech '789). Claim 28 is directed to variant polypeptides of SEQ ID NO: 13 or SEQ ID NO: 19, and claims 29 and 30 are directed to specific variants and mutants of SEQ ID NO: 19. Cech '789 generally provides variants of human telomerase catalytic subunit and a mutant plasmid in which Asp869 is

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substituted with an alanine. However, Cech '789 does not teach any sequences in which Asp868 is changed to the amino acid alanine. The Examiner points to column 198, line 14-15 of Cech '789 to support her statements, but that portion of Cech '789 provides SEQ ID NOS: 51, 52 and 53 which are 55, 34 and 35 amino acids in length, respectively. Therefore, amended claims 28-30 are directed to variant and mutant nucleic acids in which the codon for Asp838, is changed to the amino acid alanine and are not anticipated by Cech '769. Thus, the rejection of claims 28-30 under 35 U.S.C. § 102(e) should be withdrawn.

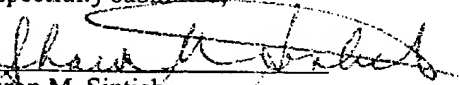
On page 7 of the Action, the Examiner stated that SEQ ID NO: 13 contains the same additional 12 nucleotides at the 5' end as SEQ ID NO: 19 and these 12 nucleotides are not identical to SEQ ID NO: 224 in Cech '836. However, this statement is incorrect; nucleotides 12-2848 SEQ ID NO: 13 are identical to nucleotides 1-2837 of SEQ ID NO: 224 of Cech '836.

CONCLUSION

In view of the foregoing amendment and remarks, Applicants believe claims 1, 2, 5, 7, 8, 11, 13, 14, 17, 26-30 and 33 are in condition for allowance and early notice thereof is requested.

Dated: August 21, 2006

Respectfully submitted,

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Blast Result

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

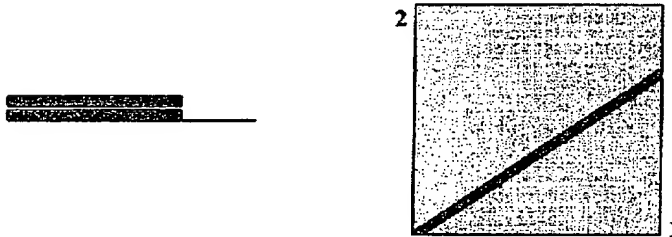
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☐ View option
 Masking character option ☒ X for protein, n for nucleotide Masking color option
☐ Show CDS translation

Sequence 1: lcl|1_seq_1
 Length = 2848 (1 .. 2848)

SEQ ID NO:3 (08/951,773)

Sequence 2: lcl|2_seq_2
 Length = 4015 (1 .. 4015)

SEQ ID NO:224 (Cech '789)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Query 12 GCAGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCC 71

Score = 5455 bits (2837), Expect = 0.0
 Identities = 2837/2837 (100%), Gaps = 0/2837 (0%)
 Strand=Plus/Plus

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Query	132	GCCGCTGGCCACGTTGCTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGG	191
Sbjct	121	GCCGCTGGCCACGTTGCTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGG	180

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	192	GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCCTGGTGTGCGTGCCCTGGGACGC	251
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Query	252	ACGGCCGCCCCCGCGCCCCCTCCTTCGCGCAGGTGTCTGCCTGAAGGAGCTGGTGGC	311
Sbjct	241	ACGGCCGCCCCCGCGCCCCCTCCTTCGCGCAGGTGTCTGCCTGAAGGAGCTGGTGGC	300
Query	312	CCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGCTTCGC	371
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Query	612	TCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGG	671
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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	1092	GCCCTCCTTCCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA	1151
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Query	1272	GTGCCCCACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCCCCAGC	1331
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Sbjct	1621	GAGCCCAGGGGTGGCTGTGTTCCGGCCGAGAGCACCCTCTGCGTGAGGAGATCCTGGC	1680
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Sbjct	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA	1740
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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Blast Result

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1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

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S1: 15 (29.5 bits)
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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Blast Result

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

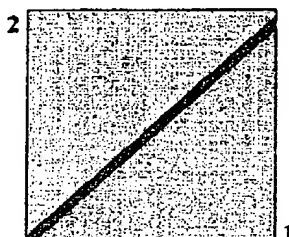
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]

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Masking character option ☒ for protein, n for nucleotide Masking color option
☐ Show CDS translation

Sequence 1: lcl|1_seq_1
Length = 3798 (1 .. 3798) SEQ ID NO: 19 (08/951,773)

Sequence 2: lcl|2_seq_2
Length = 4015 (1 .. 4015) SEQ ID NO: 224 (Cach '789)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 7274 bits (3783), Expect = 0.0
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Strand=Plus/Plus

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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	193	GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCCTGGTGTGCGTGCCCTGGGACGC	252
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Sbjct	421	CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG	480
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<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	1093	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGGA	1152
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Sbjct	1141	GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGCCT	1200
Query	1213	GCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCA	1272
Sbjct	1201	GCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACACGCGCA	1260
Query	1273	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCAGC	1332
Sbjct	1261	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCAGC	1320
Query	1333	AGCCGGTGCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGA	1392
Sbjct	1321	AGCCGGTGCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGA	1380
Query	1393	CACAGACCCCCGTCGCTGCTGTCAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGTGTA	1452
Sbjct	1381	CACAGACCCCCGTCGCTGCTGTCAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGTGTA	1440
Query	1453	CGGCTTCGTGCGGGCTGCTGCGCCGGCTGGTGCCCCAGGGCTCTGGGGCTCCAGGCA	1512
Sbjct	1441	CGGCTTCGTGCGGGCTGCTGCGCCGGCTGGTGCCCCAGGGCTCTGGGGCTCCAGGCA	1500
Query	1513	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1572
Sbjct	1501	CAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTGGGGAAGCATGCCAA	1560
Query	1573	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG	1632
Sbjct	1561	GCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAG	1620
Query	1633	GAGCCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCCTCTGCGTGAGGAGATCCTGGC	1692
Sbjct	1621	GAGCCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCACCCTCTGCGTGAGGAGATCCTGGC	1680
Query	1693	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA	1752
Sbjct	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTA	1740
Query	1753	TGTCACGGAGACCAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1812
Sbjct	1741	TGTCACGGAGACCAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
Query	1813	CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACGCTGCGGGAGCTGTC	1872
Sbjct	1801	CAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACGCTGCGGGAGCTGTC	1860
Query	1873	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1932
Sbjct	1861	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
Query	1933	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC	1992
Sbjct	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGC	1980

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	1993	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2052
Sbjct	1981	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
Query	2053	CAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG	2112
Sbjct	2041	CAGCGTGCTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGGCGCCTCTGTGCTGGG	2100
Query	2113	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCC	2172
Sbjct	2101	CCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCC	2160
Query	2173	GCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA	2232
Sbjct	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA	2220
Query	2233	GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAACCCAGAACACGTAAGCGTGCG	2292
Sbjct	2221	GGACAGGCTCAGGAGGTTCATCGCCAGCATCATCAAACCCAGAACACGTAAGCGTGCG	2280
Query	2293	TCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGACAGTCCGCAAGGCCTTCAAGAGCCA	2352
Sbjct	2281	TCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGACAGTCCGCAAGGCCTTCAAGAGCCA	2340
Query	2353	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2412
Sbjct	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGA	2400
Query	2413	GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2472
Sbjct	2401	GACCAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
Query	2473	CAGTGGCCTCTTCGACGCTCTTCTACGCTTCATGTGCCACACGCCGTGCGCATCAGGGG	2532
Sbjct	2461	CAGTGGCCTCTTCGACGCTCTTCTACGCTTCATGTGCCACACGCCGTGCGCATCAGGGG	2520
Query	2533	CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2592
Sbjct	2521	CAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
Query	2593	CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGCGGGGATTGGCGGGACGGGCT	2652
Sbjct	2581	CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGCGGGGATTGGCGGGACGGGCT	2640
Query	2653	GCTCCTGCGTTTGGTGGATGATTTCTTGTGTTGGTGACACCTCACCTACCCACGCGAAAC	2712
Sbjct	2641	GCTCCTGCGTTTGGTGGATGATTTCTTGTGTTGGTGACACCTCACCTACCCACGCGAAAC	2700
Query	2713	CTTCCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTGCGGAA	2772
Sbjct	2701	CTTCCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTGCGGAA	2760
Query	2773	GACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2832
Sbjct	2761	GACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
Query	2833	GCCGGCCACGGCCTATTCCCCTGGTGCGGCCCTGCTGCTGGATACCCGACCCCTGGAGGT	2892
Sbjct	2821	GCCGGCCACGGCCTATTCCCCTGGTGCGGCCCTGCTGCTGGATACCCGACCCCTGGAGGT	2880

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	2893	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2952
Sbjct	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Query	2953	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3012
Sbjct	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
Query	3013	TCACAGCCTGTTTCTGGATTGTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3072
Sbjct	3001	TCACAGCCTGTTTCTGGATTGTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3060
Query	3073	CAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTC	3132
Sbjct	3061	CAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTC	3120
Query	3133	TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCT	3192
Sbjct	3121	TCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCT	3180
Query	3193	CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGC	3252
Sbjct	3181	CTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGC	3240
Query	3253	CGGCCCTCTGCCCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCT	3312
Sbjct	3241	CGGCCCTCTGCCCTCCGAGGCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCT	3300
Query	3313	GACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCA	3372
Sbjct	3301	GACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCA	3360
Query	3373	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAACCGGC	3432
Sbjct	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAACCGGC	3420
Query	3433	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3492
Sbjct	3421	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
Query	3493	GAGCAGACACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGCGGCC	3552
Sbjct	3481	GAGCAGACACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGCGGCC	3540
Query	3553	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCTG	3612
Sbjct	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCTG	3600
Query	3613	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT	3672
Sbjct	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCT	3660
Query	3673	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3732
Sbjct	3661	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCA	3720
Query	3733	GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3792
Sbjct	3721	GGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query 3793 CCTGAT 3798
|| |||
Sbjct 3781 CCAGAT 3786

CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 1326
Number of extensions: 40
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 3798
Length of database: 17,737,237,516
Length adjustment: 27
Effective length of query: 3771
Effective length of database: 17,737,237,489
Effective search space: 66887122571019
Effective search space used: 66887122571019
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 15 (29.5 bits)
S2: 22 (43.0 bits)

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Blast Result

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**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

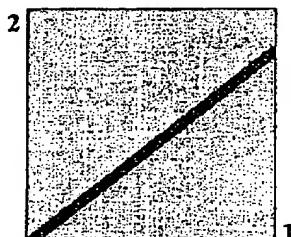
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: **lc|1_seq_1**
Length = 949 (1 .. 949)

SEQ ID NO: 14 (08/15/773)

Sequence 2: **lc|2_seq_2**
Length = 1132 (1 .. 1132)

SEQ ID NO: 225 (Cech '78)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1892 bits (4900), Expect = 0.0
Identities = 927/927 (100%), Positives = 927/927 (100%), Gaps = 0/927 (0%)

Query	23	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAAFRALVAQCLVCVPW	82
		MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAAFRALVAQCLVCVPW	
Sbjct	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAAFRALVAQCLVCVPW	60
Query	83	DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	142
		DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	
Sbjct	61	DARPPPAAPSFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	120
Query	143	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	202
		SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	
Sbjct	121	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	180
Query	203	ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR	262
		ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR	
Sbjct	181	ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR	240

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Query	263	GAAPEPERTPVGQGSWAHPGTRGSPDRGFCVVS	PARPAEEATSLEGALSGTRHSHPSVG	322
Sbjct	241	GAAPEPERTPVGQGSWAHPGTRGSPDRGFCVVS	PARPAEEATSLEGALSGTRHSHPSVG	300
Query	323	RQHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL		382
Sbjct	301	RQHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL		360
Query	383	VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT		442
Sbjct	361	VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT		420
Query	443	PAAGVCAREKPGQGSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS		502
Sbjct	421	PAAGVCAREKPGQGSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS		480
Query	503	RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI		562
Sbjct	481	RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI		540
Query	563	LAKFLHWLMSVYVVVELLRSFFYVTETTFQKNRLLFPYRKSVWSKLQSIGIRQHLKRVQLRE		622
Sbjct	541	LAKFLHWLMSVYVVVELLRSFFYVTETTFQKNRLLFPYRKSVWSKLQSIGIRQHLKRVQLRE		600
Query	623	LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA		682
Sbjct	601	LSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA		660
Query	683	LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI		742
Sbjct	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI		720
Query	743	PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAPKSHVSTLTDLPYMRQFVAHL		802
Sbjct	721	PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAPKSHVSTLTDLPYMRQFVAHL		780
Query	803	QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSILSTL		862
Sbjct	781	QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSILSTL		840
Query	863	LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL		922
Sbjct	841	LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL		900
Query	923	RKTVVNFPVEDEALGGTAFVQMPAHGL		949
Sbjct	901	RKTVVNFPVEDEALGGTAFVQMPAHGL		927

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.324	0.136	0.438

Gapped		
Lambda	K	H
0.267	0.0410	0.140

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 9263
Number of extensions: 5430
Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 1
Length of query: 949
Length of database: 1,308,253,377
Length adjustment: 144
Effective length of query: 805
Effective length of database: 1,308,253,233
Effective search space: 1053143852565
Effective search space used: 1053143852565
Neighboring words threshold: 9
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 84 (37.0 bits)

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Blast Result

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**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

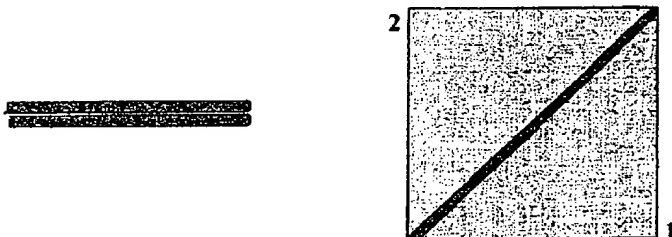
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|1_seq_1
Length = 1154 (1 .. 1154)

SEQ ID NO: 20 (08/951,773)

Sequence 2: lcl|2_seq_2
Length = 1132 (1 .. 1132)

SEQ ID NO: 225 (Cech-789)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2300 bits (5961), Expect = 0.0
Identities = 1132/1132 (100%), Positives = 1132/1132 (100%), Gaps = 0/1132 (0%)

Query	23	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAAFRALVAQCLVCVPW	82
		MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAAFRALVAQCLVCVPW	
Sbjct	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPQGWRLVQRGDPAAAFRALVAQCLVCVPW	60
Query	83	DARPPPAAPSFRQVSKLVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	142
		DARPPPAAPSFRQVSKLVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	
Sbjct	61	DARPPPAAPSFRQVSKLVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR	120
Query	143	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	202
		SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	
Sbjct	121	SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
Query	203	ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR	262
		ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR	
Sbjct	181	ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKRPRR	240

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Blast Result

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Query	263	GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVS	PARPAEEATSLEGALSGTRHSHPSVG	322	
Sbjct	241	GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVS	PARPAEEATSLEGALSGTRHSHPSVG	300	
Query	323	RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDK	EQLRPSFLLSSLRPSLTGARRL	382	
Sbjct	301	RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDK	EQLRPSFLLSSLRPSLTGARRL	360	
Query	383	VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGN	HAQCPYGVLLKTHCPLRAAVT	442	
Sbjct	361	VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGN	HAQCPYGVLLKTHCPLRAAVT	420	
Query	443	PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS		502	
Sbjct	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS		480	
Query	503	RHNERRFLRNTKKFISLGKHA	KLSQLTWMKSVRDCAWLRSPGVGCVPAAEHRLREEI	562	
Sbjct	481	RHNERRFLRNTKKFISLGKHA	KLSQLTWMKSVRDCAWLRSPGVGCVPAAEHRLREEI	540	
Query	563	LAKFLHWLMSVYVVELLR	SFFYVTETTFQKNR	LFYRKSVWSKLQSIGIRQHLKRVOLRE	622
Sbjct	541	LAKFLHWLMSVYVVELLR	SFFYVTETTFQKNR	LFYRKSVWSKLQSIGIRQHLKRVOLRE	600
Query	623	LSEAEVRQHREAR	PALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	682	
Sbjct	601	LSEAEVRQHREAR	PALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660	
Query	683	LFSVLNYERARRPGLLGASVLGLDDI	HRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI	742	
Sbjct	661	LFSVLNYERARRPGLLGASVLGLDDI	HRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720	
Query	743	PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTL	TDLPYMRQFVAHL	802	
Sbjct	721	PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTL	TDLPYMRQFVAHL	780	
Query	803	QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI	PQGSILSTL	862	
Sbjct	781	QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI	PQGSILSTL	840	
Query	863	LCSLCYGDMENKLFAGIRRDG	LLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL	922	
Sbjct	841	LCSLCYGDMENKLFAGIRRDG	LLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL	900	
Query	923	RKTVVNFVFEDEALGGTAFVQMPAHGLFPWCGLLLD	TRTLEVQSDYSSYARTSIRASLTF	982	
Sbjct	901	RKTVVNFVFEDEALGGTAFVQMPAHGLFPWCGLLLD	TRTLEVQSDYSSYARTSIRASLTF	960	
Query	983	NRGFKAGRNMRRLFGVLR	RLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1042	
Sbjct	961	NRGFKAGRNMRRLFGVLR	RLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020	
Query	1043	FHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL		1102	
Sbjct	1021	FHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL		1080	
Query	1103	KLTRHRVTYVPLGSLR	TAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD	1154	
Sbjct	1081	KLTRHRVTYVPLGSLR	TAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD	1132	

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?0>

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Blast Result

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CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda	K	H
0.324	0.138	0.434

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 10,897
Number of extensions: 6421
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1154
Length of database: 1,308,253,377
Length adjustment: 145
Effective length of query: 1009
Effective length of database: 1,308,253,232
Effective search space: 1320027511088
Effective search space used: 1320027511088
Neighboring words threshold: 9
X1: 15 (7.0 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 40 (21.6 bits)
S2: 84 (37.0 bits)

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